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☐ 1: AAD05421. NADH:ubiquinone o...[gi:4164446]   BLink, Links

```
LOCUS       AAD05421                 129 aa            linear   PRI 19-JAN-1999
DEFINITION  NADH:ubiquinone oxidoreductase B15 subunit [Homo sapiens].
ACCESSION   AAD05421
VERSION     AAD05421.1  GI:4164446
DBSOURCE    locus AF044957 accession AF044957.1
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 129)
  AUTHORS   Loeffen,J.L., Triepels,R.H., van den Heuvel,L.P., Schuelke,M.,
            Buskens,C.A., Smeets,R.J., Trijbels,J.M. and Smeitink,J.A.
  TITLE     cDNA of eight nuclear encoded subunits of NADH:ubiquinone
            oxidoreductase: human complex I cDNA characterization completed
  JOURNAL   Biochem. Biophys. Res. Commun. 253 (2), 415-422 (1998)
  MEDLINE   99097250
   PUBMED   9878551
REFERENCE   2  (residues 1 to 129)
  AUTHORS   Triepels,R., Loeffen,J., van den Heuvel,B., Schuelke,M.,
            Buskens,C., Smeets,R., Trijbels,F. and Smeitink,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-1998) Nijmegen Center for Mitochondrial
            Disorders, University Hospital Nijmegen, P.O. Box 9101, Nijmegen,
            Gelderland 6500 HB, Netherlands
COMMENT     Method: conceptual translation supplied by author.
FEATURES             Location/Qualifiers
     source          1..129
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     Protein         1..129
                     /product="NADH:ubiquinone oxidoreductase B15 subunit"
                     /name="complex I subunit"
     CDS             1..129
                     /coded_by="AF044957.1:9..398"
                     /note="NDUFB4 subunit"
ORIGIN
        1 msfpkykpss lrtlpetldp aeynispetr raqaerlair aqlkreyllq yndpnrrgli
       61 enpallrway artinvypnf rptpknslmg alcgfgplif iyyiikterd rkekliqegk
      121 ldrtfhlsy
//
```

Apr 28 2003 10:17:55

Docket No.: PF-0187-2 RCE
USSN: 09/726,899
Encl. No. _2_ of _3_

4/28/03 3:29

```
Score = 268 bits (678), Expect = 4e-71
Identities = 129/129 (100%), Positives = 129/129 (100%)

Query: 1   MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLI 60
           MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLI
Sbjct: 1   MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLI 60

Query: 61  ENPALLRWAYARTINVYPNFRPTFKNSLWGALCGPGLPIFYYIIKTEDRKEKLIQPGK 120
           ENPALLRWAYARTINVYPNFRPTFKNSLWGALCGPGLPIFYYIIKTEDRKEKLIQPGK
Sbjct: 61  ENPALLRWAYARTINVYPNFRPTFKNSLWGALCGPGLPIFYYIIKTEDRKEKLIQPGK 120

Query: 121 LDRTFHLSY 129
           LDRTFHLSY
Sbjct: 121 LDRTFHLSY 129
```

>g12654091 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4
(15kD, B15) [Homo sapiens]
Length = 129

```
Score = 268 bits (678), Expect = 4e-71
Identities = 129/129 (100%), Positives = 129/129 (100%)

Query: 1   MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLI 60
           MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLI
Sbjct: 1   MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLI 60

Query: 61  ENPALLRWAYARTINVYPNFRPTFKNSLWGALCGPGLPIFYYIIKTEDRKEKLIQPGK 120
           ENPALLRWAYARTINVYPNFRPTFKNSLWGALCGPGLPIFYYIIKTEDRKEKLIQPGK
Sbjct: 61  ENPALLRWAYARTINVYPNFRPTFKNSLWGALCGPGLPIFYYIIKTEDRKEKLIQPGK 120

Query: 121 LDRTFHLSY 129
           LDRTFHLSY
Sbjct: 121 LDRTFHLSY 129
```

>g21961389 Unknown (protein for IMAGE:5165512) [Homo sapiens]
Length = 119

```
Score = 226 bits (569), Expect = 2e-58
Identities = 108/108 (100%), Positives = 108/108 (100%)

Query: 2   SFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLIE 61
           SFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLIE
Sbjct: 1   SFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLIE 60

Query: 62  NPALLRWAYARTINVYPNFRPTFKNSLWGALCGPGLPIFYYIIKTER 109
           NPALLRWAYARTINVYPNFRPTFKNSLWGALCGPGLPIFYYIIKTER
Sbjct: 61  NPALLRWAYARTINVYPNFRPTFKNSLWGALCGPGLPIFYYIIKTER 108
```

>g12858553 unnamed protein product [Mus musculus]
Length = 129

```
Score = 210 bits (529), Expect = 1e-53
Identities = 97/129 (75%), Positives = 113/129 (87%)

Query: 1   MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLREYLLQYNDPNRRGLI 60
```

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| BLAST2 Manual |

Confidential -- Property of Incyte Genomics, Inc.   SeqServer Version 4.8 Jan 2002

Program: blastp
Sequence ID(s):
  1600202CD1_SEQIDNO:3 vs. genpept134

NCBI-BLASTP 2.0.10 (Aug-26-1999)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

Query= 1600202CD1_SEQIDNO:3
         (129 letters)

Database: genpept134
         1,315,470 sequences; 407,408,102 total letters

Searching...done

Sequences producing significant alignments:	Score (bits)	E Value
g4164446 NADH:ubiquinone oxidoreductase B15 subunit [Homo sap	268	4e-71
g12654091 NADH dehydrogenase (ubiquinone) 1 beta subcomplex,	268	4e-71
g21961389 Unknown (protein for IMAGE:5165512) [Homo sapiens]	226	2e-58
g12858553 unnamed protein product [Mus musculus]	210	1e-53
g12844810 unnamed protein product [Mus musculus]	210	1e-53
g28189196 similar to B15 subunit of the NADH: ubiquinone oxid	204	7e-52
g114_B15 subunit of the NADH: ubiquinone oxidoreductase compl	204	7e-52
g28189643 similar to B15 subunit of the NADH: ubiquinone oxid	147	9e-35
g12836527 unnamed protein product [Mus musculus]	94	2e-18
g512250 hypothetical protein walter (Gallus gallus)	62	4e-09

>g4164446 NADH:ubiquinone oxidoreductase B15 subunit [Homo sapiens]
Length = 129

4/28/03 3:29 PM   2 of 5

```
                                                                MS  KYKP+ L TLP TLDPAEY++SPETRRAQ ERL+IRA+LKREYLLQYNDP R  I
Sbjct: 1                                                        MSFPKYEASRLSSLPTTLDPAEYDVSPETRRAQVERLSIRARLREYKYQLQYYDPSRRGVI 60

Query: 61   ENPALLRWAYARTINVYNFRPTFRNSLWQALCGPGPLIFYYILIKTEDRREKLIQEEK 120
Sbjct: 61   EDPALVRWTYARSANIYPNFRPTFKNSLLGAVAGPGPLIFWYYVFKTDDRREKLIQEEK 120

Query: 121  LDRTFHLSY 129
Sbjct: 121  LDRKFNISY 129
```

```
>gi2844810 unnamed protein product [Mus musculus]
            Length = 129

 Score =  210 bits (529), Expect = 1e-53
 Identities = 97/129 (75%), Positives = 113/129 (87%)

Query: 1    MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQERLAIRAQLKREYLLQYNDPQ R  I
Sbjct: 1    MS  KYKP+ L TLP TLDPAEY++SPETRRAQ ERL+IRA+LKREYLLQYNDP R  I
            MSGSKYKPAPLATTLPSTLDPAEYDVSPETRRAQVERLSIRARLREYLLQYNDPKRVSHI 60

Query: 61   ENPALLRWAYARTINVYNFRPTFRNSLWQALCGPGPLIFYYILIKTEDRREKLIQEEK 120
Sbjct: 61   E+PAL+RW YAR+ N+YPNFRP+ K SL+GAL G GPGPLIF YY+ KT+DRREK+LIQEEK 120

Query: 121  LDRTFHLSY 129
Sbjct: 121  LDRKFNISY 129
```

```
>gi28189196 similar to B15 subunit of the NADH: ubiquinone
            oxidoreductase complex (Bos taurus)
            Length = 129

 Score =  204 bits (514), Expect = 7e-52
 Identities = 95/129 (73%), Positives = 113/129 (86%)

Query: 1    MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQERLAIRAQLKREYLLQYNDPNR RGLI 60
Sbjct: 1    MSFPKY+ S L +LP TLDPAEY+IS ETR+AQ ERL+IRA ++LKREY LQY DP+RRG+I
            MSFPKYEASRLSSLPTTLDPAEYDISSETRRAQVERLSIRARLREYQLQYYDPSRRGVI 60

Query: 61   ENPALLRWAYARTINVYNFRPTFRNSLWQALCGPGPLIFYYILIKTEDRREKLIQEEK 120
Sbjct: 61   EDPALVRWTYARSANIYPNFRPVKTSLLGALPGIGPLVFWYVVFKTIDRREKLIQEEK 120

Query: 121  LDRTFHLSY 129
Sbjct: 121  LDRKFNISY 129
```

```
>gi14 B15 subunit of the NADH: ubiquinone oxidoreductase complex
            (Bos taurus)
            Length = 129

 Score =  204 bits (514), Expect = 7e-52
 Identities = 95/129 (73%), Positives = 113/129 (86%)

Query: 1    MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQERLAIRAQLKREYLLQYNDPNRRGLI 60
```

```
                                                                MSFPKY+ S L +LP TLDPAEY+IS ETR+AQ ERL+IRA ++LKREY LQY DP+RRG+I
Sbjct: 1                                                        MSFPKYEASRLSSLPTTLDPAEYDISSETRRAQVERLSIRARLREYQLQYYDPSRRGVI 60

Query: 61   ENPALLRWAYARTINVYNFRPTFRNSLWQALCGPGPLIFYYILIKTEDRREKLIQEEK 120
                                                                E+PAL+RW YAR+ N+YPNFRP K SL+GAL G GPL+F YY+ KT+DRREK+LIQEEK
Sbjct: 61                                                       EDPALVRWTYARSANIYPNFRPVKTSLLGALPGIGPLVFWYVVFKTIDRREKLIQEEK 120

Query: 121  LDRTFHLSY 129
                                                                LDRTF++SY
Sbjct: 121  LDRKFNISY 129
```

```
>gi28189641 similar to B15 subunit of the NADH: ubiquinone
            oxidoreductase complex (Bos taurus)
            Length = 97

 Score =  147 bits (368), Expect = 9e-35
 Identities = 69/97 (71%), Positives = 82/97 (84%)

Query: 1    MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQERLAIRAQLKREYLLQYNDPNRRGLI 60
            MSFPKY+ S L +LP TLDPAEY+IS ETR+AQ ERL+IRA ++LKREY LQY DP R  I
Sbjct: 1    MSFPKYEASRLSSLPTTLDPAEYDISSETRRAQVERLSIRARLREYQLQYYDPSRRGVI 60

Query: 61   ENPALLRWAYARTINVYNFRPTFRNSLWQALCGPGP 97
            E+PAL+RW YAR+ N+YPNFRP K SL+GAL GP
Sbjct: 61   EDPALVRWTYARSANIYPNFRPVKTSLLGALPGIGP 97
```

```
>gi12836537 unnamed protein product [Mus musculus]
            Length = 119

 Score = 93.6 bits (229), Expect = 2e-18
 Identities = 44/56 (78%), Positives = 49/56 (86%)

Query: 1    MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQERLAIRAQLKREYLLQYNDPNR 56
            MS  KYKP+ L TLP TLDPAEYDVSPETRRAQVERLSIRARLREYLLQYNDPKR
Sbjct: 1    MSGSKYKPAPLATTLPSTLDPAEYDVSPETRRAQVERLSIRARLREYLLQYNDPKR 56
```

```
>gi17250 hypothetical protein walter (Gallus gallus)
            Length = 179

 Score = 62.5 bits (149), Expect = 4e-09
 Identities = 30/50 (60%), Positives = 38/50 (76%)

Query: 5    KYKPSSLRTLPETLDPAEYNISPETRRAQERLAIRAQLKREYLLQYNDP 54
            +Y+P+  +LP LDPA Y+  E RRA+AERLAIRA+LKR+YLLQ N P
Sbjct: 26   EYRPRVYSLPAELDPATYDTFLKRRARAERLAIRARLRQYLLQLNTP 75
```

```
Database: genpept134
  Posted date: Feb 28, 2003  2:38 PM
Number of letters in database: 407,408,102
Number of sequences in database: 1,315,470

Lambda     K       H
  0.321   0.140   0.416

Gapped
```

```
Lambda      K        H
  0.270   0.0470   0.230
```

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 110103617
Number of Sequences: 1315470
Number of extensions: 4259804
Number of successful extensions: 7863
Number of sequences better than 10.0: 17
Number of HSP's better than 10.0 without gapping: 15
Number of HSP's successfully gapped in prelim test: 2
Number of HSP's that attempted gapping in prelim test: 7848
Number of HSP's gapped (non-prelim): 17
length of query: 129
length of database: 407,408,102
effective HSP length: 52
effective length of query: 77
effective length of database: 339,003,662
effective search space: 26103281974
effective search space used: 26103281974
T: 11
A: 40
X1: 16  ( 7.4 bits)
X2: 38  (14.8 bits)
X3: 64  (24.9 bits)
S1: 41  (21.8 bits)
```

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